

**AMENDMENTS TO THE SPECIFICATION**

Please amend the specification as follows:

Please replace Table 1 spanning pages 7-8 with the following new Table 1 below, which corrects line spacing in the table only:

**Table 1**

<b>Amino Acid</b>	<b>One-Letter Abbreviation</b>	<b>Three-Letter Abbreviation</b>
Alanine	A	Ala
Arginine	R	Arg
Asparagine	N	Asn
Aspartic Acid	D	Asp
Cysteine	C	Cys
Glutamine	Q	Gln
Glutamic Acid	E	Glu
Glycine	G	Gly
Histidine	H	His
Isoleucine	I	Ile
Leucine	L	Leu
Lysine	K	Lys
Methionine	M	Met
Phenylalanine	F	Phe
Proline	P	Pro
Serine	S	Ser
Threonine	T	Thr
Tryptophan	W	Trp
Tyrosine	Y	Tyr
Valine	V	Val

Please replace Table 2, beginning on page 18, line 13, with the following new Table 2 shown below, which corrects line spacing in the table only (no additions or deletions to the amino acid sequences are to be made to Table 2):

**Table 2**

**Amino Acid Sequences of Edg Receptors**

	MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNITGKLNISAD
Human Edg 1	KENSIKLT <u>SVVFILICCFIILENIFVLLTIWKTKKFHRPM</u>
(SEQ ID NO: 1)	<u>YYFIGNLALSDDL</u> AGVAYTANLLLSGATTYKLTPAQWFLR
	EGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRL
Genbank	<u>FLLISACWVISLILGGLPIMGWNCISALSSCSTVLP</u> LYHK
Accession No.	<u>HYILFCTTVFTLLLSIVILYCRIYSLVRTRSRRLTFRKN</u>
AF233365	<u>ISKASRSSEKSLALLKT</u> VIIIVLSVFIACWAPLFILLLLDV
	GCKVKTCDILFRAEYFLVLAVLNSGTNP <sup>II</sup> YT <sup>L</sup> TNKEMRR
	AFIRIMSCCKCPSGDSAGKFKRPIIAGMEFSRSKSDNSSH
	PQKDEGDNPETIMSSGNVNSSS
Human Edg 2	MAAISTSI <sup>P</sup> VISQPQFTAMNEPQCFYNESIAFFYNRSGKH
(SEQ ID NO: 30)	LATEWNTVSKLVMGLGITVCIFIMLANLLVMVAI <sup>Y</sup> VNRRF
	<u>HFPIYYLMANLAAADFFAGLAYFYLMFNTGP</u> NTRRLTVST
Genbank	<u>WLLRQGLIDTSLTASVANLLAIAIERHITVFRMQLHTRMS</u>
Accession	<u>NRRVVVVIVVIWTMAIVMGAIPSVGWNCICDIENCSNMAP</u>
No. U78192	<u>LYSDSYLVFWAIFNLVTFVVMVVL</u> YAHIFGYVRQRTMRMS
	<u>RHSSGPRRNRDTMMSLLKT</u> VVIVLGAFIICWTPGLVLLLL
	<u>DVCCPQCDVLAYEKFFLL</u> AEFNSAMNP <sup>II</sup> YSYRDKEMSA
	TFRQILCCQRSENPTGPTEGSDRSASSLNHTILAGVHSND
	HSV <sup>V</sup>

Human Edg 3                    MATALPPRLQPVRGNETLREHYQYVGKLAGRLKEASEGST  
(SEQ ID NO: 2)                LTTVLFLVICSFIVLENLMVLIAIWKNNKFHNRMYFFIGN  
                                 LALCDLLAGIAYKVNILMSGKKTFSLSPTVWFLREGSMFV  
Genbank                        ALGASTCSLLAIAIERHLTMIKMRPYDANKRHRVFLIGM  
Accession No.                CWLIAFTLGALPILGWNCLHNLPCSTILPLYSKKYIAFC  
X83864                        ISIFTAILVTIVILYARIYFLVKSSSRKVANHNNSERSMA  
                                 LLRTVVIVVSVFIACWSPLFILFLIDVACRVQACPILFKA  
                                 QWFIVLAVLNSAMNPVIYTLASKEMRRAFFRLVCNCLVRG  
                                 RGARASPIQPALDPSRSKSSSSNNSSHSPKVKEDLPHTDP  
                                 SSCIMDKNAALQNGIFCN

Human Edg 4                    MVIMGQCYINETIGFFYNNSGKELSSHWRPKDVVVVALGL  
(SEQ ID NO: 31)                TVSVLVLLTNLLVIAAIASNRRFHQPIYYLLGNLAAADLF  
                                 AGVAYLFLMFHTGPRTARLSLEGWFLRQGLDTSLTASVA  
Genbank                        TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALG  
Accession No.                LGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLV  
AF233092                        FLLMVAVYTRI FFYVRRRVQORMAEHVSCHPRYRETTLSLV  
                                 KTVV IILGAFVVCWTPGQVVLLLDGLGCESC NVLAVEKYF  
                                 LLAEANSLVNAAVYSCRDAEMRRTFRRLCCACLRQSTR  
                                 ESVHYTSSAQGGASTRIMLPENGHPLMDSTL

Human Edg 4 mt                MVIMGQCYINETIGFFYNNSGKELSSHWRPKDVVVVALGL  
(SEQ ID NO:32)                TVSVLVLLTNLLVIAAIASNRRFHQPIYYLLGNLAAADLF  
                                 AGVAYLFLMFHTGPRTARLSLEGWFLRQGLDTSLTASVA  
Genbank                        TLLAIAVERHRSVMAVQLHSRLPRGRVVMLIVGVVVAALG  
Accession No.                LGLLPAHSWHCLCALDRCSRMAPLLSRSYLAVWALSSLLV  
AF011466                        FLLMVAVYTRI FFYVRRRVQORMAEHVSCHPRYRETTLSLV  
                                 KTVV IILGAFVVCWTPGQVVLLLDGLGCESC NVLAVEKYF

LLLAEANSLVNAAVYSCRDAEMRRTFRRLCCACLRQSTR  
ESVHYTSSAQGGASTRIMLPENGHPLMTPPFSYLELQRYA  
ASNKSTAPDDLWVLLAQPNQQD

Human Edg 5      MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFI  
(SEQ ID NO: 33)   VILCCAIVVENLLVLIAVARNSKFHSAMYLFLGNLASDL  
LAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV  
Genbank            FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISL  
Accession No.    VLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI  
AF034780          ILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG  
VFIVCWLPAFSILLDYACPVHSCPILYKAHYFFAVSTLN  
SLLNPVIYTWRSRDLRREVLRPLQCWRPGVGVQGRRRVGT  
PGHHLLPLRSSSSLERGMHMPTSPTFLEGNTVV

Human Edg 6      MNATGTPVAPESCQQLAAGGHSRLIVLHYNHSGRLAGRGG  
(SEQ ID NO: 34)   PEDGGLGALRGLSVAASCLVVENLLVLAAITSHMRSRRW  
Genbank            VYYCLVNITLSDLLTGAAYLANVLLSGARTFRLAPAQWFL  
Accession No.    REGLLFTALAASTFSLLFTAGERFATMVRPVAESGATKTS  
AJ000479          RVYGFIGLCWLLAALLGMLPLLGWNCLCAFDRCSSLLPLY  
SKRYILFCLVIFAGVLATIMGLYGAIFRLVQASGQKAPRP  
AARRKARRLLKTVLMILLAFLVCWGPLFGLLLADVFGSNL  
WAQEYLRGMDWILALAVLNSAVNPIIYSFRSREVCRAVLS  
FLCCGCLRLGMRGPGDCLARAVEAHSGASTDSSLRPRDS  
FRGSRSLSFRMREPLSSISSVRSI

Human Edg 7      MNECHYDKHMDFFYNRSNTDTVDDWTGTKLVIVLCVGTFF  
SEQ ID NO: 35)   CLFIFFSNSLVIAAVIKNRKFHFPFYYLLANLAADFFAG  
Genbank            IAYVFLMFNTGPVSKTLTVNRWFLRQGLLDSSLTASLTNL

Accession No. LVIAVERHMSIMRMRVHSNLTKKRVTLLILLVWAIAIFMG  
AF127138 AVPTLGWNCLCNISACSSLAPIYSRSYLVFWTVSNLMAFL  
IMVVVYLRIYVYVKRKTNVLSPHTSGSISRRRTPMKLMKT  
VMTVLGAFVVCWTPGLVVLLLDGLNCRQCGVQHVKRWFL  
LALLNSVVNPIIYSYKDEDMYGTMKKMICCFSQENPERRP  
SRIPSTVLSRSDTGSQYIEDSISQGAVCNKSTS

Human Edg 8 MESGLLRPAPVSEVIVLHYNITGKLRGARYQPGAGLRADA  
(SEQ ID NO: 36) VVCLAVCAFIVLENLAVLLVLGRHPRFHAPMFLLLGSLTL  
Genbank SDLLAGAAYAANILLSGPLTLKLSPALWFAREGGVFVALT  
Accession No. ASVLSLLAIALERSLTMARRGPAPVSSRGRTLAMAAAAWG  
AF317676 VSLLLGLLPALGWNCLGRLDACSTVLPLYAKAYVLFCVLA  
FVGILAAICALYARIYCQVRANARRLPARPGTAGTTSTRA  
RRKPRSLALLRTLSVVLLAFVACWGPLFLLLLLDVACPAR  
TCPVLLQADPFLGLAMANSLLNPIIYTLTNRDLRHALLRL  
VCCGRHSCGRDPSGSQQSASAAEASGGLRRCLPPGLDGSF  
SGSERSSPQRDGLDTSGSTGSPGAPTAARTLVSEPAAD

Please replace Table 3, beginning on page 21, line 1 with new Table 3 shown below, which corrects line spacing in the table only (no additions or deletions to the amino acid sequences are to be made to Table 3):

**Table 3**

**Amino Acid Sequences of Chimeric Edg Receptors**

Edg1/3(ct)	MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNITGKLNISAD
(SEQ ID NO: 3)	KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM
	YYFIGNLALSDDLAVAYTANLLLSGATTYKLTPAQWFLR
	EGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRL
	FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK
	HYILFCTTVFTLLLLSIVILYCRIYSLVRTRSRRLTFRKN
	ISKASRSSEKSLALLKTVIIVLSVFIACWAPLFILLLLDV
	GCKVKTCDILFRAEYFLVLAVLNSGTNP IIYTLTSKEMRR
	<b>AFFRLVCNCLVRGRGARASPIQPALDPSRSKSSSSNNSSH</b>
	<b>SPKVKEDLPHTDPSSCIMDKNAALQNGIFCN</b>

Edgl/3(i3ct)  
(SEQ ID NO: 4) MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISAD  
KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM  
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLR  
EGSMFVALSASVFSLLAIAIERYITMLKMKLHNGSNNFRL  
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK  
HYILFCTTVFTLLLLSIVILYCRIYSLVR**SSSRKVANHNN**  
**SERSMALLRTV**IIVLSVFIACWAPLFILLLLDVGCKVKTC  
DILFRAEYFLVLAVLNSGTNP I IYTLT**SKEMRRAFFRLVC**  
**NCLVRGRGARASPIQPALDPSRSKSSSSNNSSHSPKVKE**  
**LPHTDPSSCIMDKNAALQNGIFCN**

Edgl/3(i2i3ct)  
(SEQ ID NO:5) MGPTSVPLVKAHRSSVSDYVNYDIIVRHYNYTGKLNISAD  
KENSIKLTSVVFILICCFIILENIFVLLTIWKTKKFHRPM  
YYFIGNLALSDLLAGVAYTANLLLSGATTYKLTPAQWFLR  
EGSMFVALSASVFSLLAIAIAI**ERHLTMIKMRPYDANKRHRL**  
FLLISACWVISLILGGLPIMGWNCISALSSCSTVLPLYHK  
HYILFCTTVFTLLLLSIVILYCRIYSLVR**SSSRKVANHNN**  
**SERSMALLRTV**IIVLSVFIACWAPLFILLLLDVGCKVKTC  
DILFRAEYFLVLAVLNSGTNP I IYTLT**SKEMRRAFFRLVC**  
**NCLVRGRGARASPIQPALDPSRSKSSSSNNSSHSPKVKE**  
**LPHTDPSSCIMDKNAALQNGIFCN**

Edg 5/3(i3ct)  
(SEQ ID NO:37) MGSLYSEYLNPNKVQEHYNYTKETLETQETTSRQVASAFI  
VILCCAIVVENLLVLIAVARN**SKFHS**AMYLFLGNLAASDL  
LAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV

FSLLAIAIERHVAIAKVKLYGSDKSCRMLLLIGASWLISL  
VLGGLPILGWNCLGHLEACSTVLPLYAKHYVLCVVTIFSI  
ILLAIVALYVRIYCVV**KSSSRKVANHNNSESMALLRTVT**  
IVLGVFIVCWLPAFSILLDDYACPVHSCPILYKAHYFFAV  
STLNSSLNPVIYTW**ASKEMRRAFFRLVCNCLVRGRGARAS**  
**PIQPALEPSRSKSSSSNNSSHSPKVKEDLPHTDPSSCIMD**  
**KNAALQNGIFCN**

Edg8/4(ct)

(SEQ ID NO: 38)

MESGLLRPAPVSEVIVLHNYTGKLRGARYQPGAGLRADA  
VVCLAVCAFIVLENLAVLLVLGRHPRFHAPMFLLLGSLTL  
SDLLAGAAYAANILLSGPLTLKLSPALWFAREGGVFVALT  
ASVLSLLAIALERSLTMARRGPAPVSSRGRTLAMAAAANG  
VSLLLGLLPALGWNCLGRLDACSTVLPLYAKAYVLCVLA  
FVGILAAICALYARIYCQVRANARRLPARPGTAGTTSTRA  
RRKPRSLALLRTL SVVLLAFVACWGPFLLLLLDVACPAR  
TCPVLLQADPFLGLAMANSLLNP I IYTL**RDAEMRRTFRRL**  
**LCCACLRQSTRESVHYTSSAQGGASTRIMLPENGHPLMTP**  
**PFSYLELQRYAASNKSTAPDDLWVLLAQPNQQD**



Please replace Table 4, beginning on page 35, line 13 with new Table 4 shown below, which corrects line spacing in the table only (no additions or deletions to the amino acid sequences are to be made to Table 4):

**Table 4**

**PCR Primers for Generating Chimeric Edg 1 Receptors**

<b><u>Primer</u></b>	<b><u>Direction</u></b>	<b><u>Position</u></b>	<b><u>Sequence 5'-3'</u></b>
Edg-1 (SEQ ID NO: 6)		1	CCC/GCG/GTT/AAC/ATG/GGG/CCC/ACC/ AGC/GTC
Edg-3 (SEQ ID NO: 7)	rev	1137	CGC/GGA/TCC/TCA/GTT/GCA/GAA/GAT/ CCC
E1/3 CTD (SEQ ID NO: 8)		942	CAT/TTA/CAC/TCT/GAC/CAG/CAA/GGA/ GAT/GCG/GCG/G
E1/3 CTD (SEQ ID NO: 9)	rev	942	CCG/CAT/CTC/CTT/GCT/GGT/CAG/AGT/ GTA/AAT/GAT/G
E1/3 i2 (SEQ ID NO: 10)		402	GTC/TCC/TCG/CCA/TCG/CCA/TCG/AGC/ GGC/ACT/TGA/C
E1/3 i2 (SEQ ID NO: 11)	rev	402	GTC/AAG/TGC/CGC/TCG/ATG/GCG/ATG/ GCG/AGG/AGA
E1/3 i2 (SEQ ID NO: 12)		441	CGC/CAA/CAA/GAG/GCA/CCG/CCT/CTT/ CCT/GCT/AAT/C
E1/3 i2 (SEQ ID NO: 13)	rev	441	GAT/TAG/CAG/GAA/GAG/GCG/GTG/CCT/ CTT/GTT/GGC/G

E1/3 i3 (SEQ ID NO:14)		684	CTA/CTC/CTT/GGT/CAG/GTC/CAG/CAG/ CCG/TAA/GGT/G
E1/3 i3 (SEQ ID NO:15)	rev	684	CAC/CTT/ACG/GCT/GCT/GGA/CCT/GAC/ CAA/GGA/GTA/G
E1/3 i3 (SEQ ID NO:16)		723	CAC/TGC/TGC/GGA/CCG/TGA/TTA/TCG/ TCC/TGA/GCG/TC
E1/3 i3 (SEQ ID NO:17)	rev	723	GAC/GCT/CAG/GAC/GAT/AAT/CAC/GGT/ CCG/CAG/CAG/TG

Please replace Table 5, beginning on page 38, line 1 with new Table 5 shown below, which corrects line spacing in the table only (no additions or deletions to the amino acid sequences are to be made to Table 5):

**Table 5**  
**PCR Primers for Generating Chimeric Edg 5 Receptors**

<b><u>Primer</u></b>	<b><u>Direction</u></b>	<b><u>Position</u></b>	<b><u>Sequence 5'-3'</u></b>
Edg-5 (SEQ ID NO:18)		1	CCC/GCG/GTT/AAC/ATG/GGC/AGC/ TTG/TAC/TCG
Edg-3 (SEQ ID NO:19)	rev	1137	CGC/GGA/TCC/TCA/GTT/GCA/GAA/ GAT/CCC
E5/3 (SEQ ID NO:20)		864	CGT/CAT/CTA/CAC/GTG/GGC/CAG/ CAA/GGA/GAT/GCG/G
E5/3 (SEQ ID NO:21)	rev	864	CCG/CAT/CTC/CTT/GCT/GGC/CCA/ CGT/GTA/GAT/GAC/G
E5/3 i3 (SEQ ID NO:22)		633	CAT/CTA/C TG/CGT/GGT/CAA/GTC/ CAG/CAG/CCG/TAA/G
E5/3 i3 (SEQ ID NO:23)	rev	633	CTT/ACG/GCT/GCT/GGA/CTT/GAC/ CAC/GCA/GTA/GAT/G
E5/3 i3 (SEQ ID NO:24)		723	CAC/TGC/TGC/GGA/CCG/TGA/CCA/ TCG/TGC/TAG/GCG/TC
E1/3 i3 (SEQ ID NO:25)	rev	723	GAC/GCC/TAG/CAC/GAT/GGT/CAC/ GGT/CCG/CAG/CAG/TG

Please replace Table 6, beginning on page 39, line 8 with new Table 6 shown below, which corrects line spacing in the table only (no additions or deletions to the amino acid sequences are to be made to Table 6):

**Table 6**

**PCR Primers for Generating Chimeric Edg 8 Receptors**

<b><u>Primer</u></b>	<b><u>Direction</u></b>	<b><u>Position</u></b>	<b><u>Sequence 5'-3'</u></b>
Edg-8 (SEQ ID NO:26)		1	CCC/GCG/GTT/AAC/ATG/GAG/TCG/ GGG/CTG/CTG
Edg-4-mut (SEQ ID NO:27)	rev	1149	CGC/GGA/TCC/TCA/GTC/CTG/TTG/ GTT/GGG
E8/4 (SEQ ID NO:28)		920	CCA/TCA/TCT/ACA/CGC/TCC/GAG/ ATG/CTG/AGA/TGC/G
E8/4 (SEQ ID NO:29)	rev	920	CGC/ATC/TCA/GCA/TCT/CGG/AGC/ GTG/TAG/ATG/ATG/G